Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	7	"1002862".pn.	EPO; DERWENT	OR	OFF	2005/02/01 12:30
L2	2	KIAA near5 prostate	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:31
L3	0	seladin-1 near5 prostate	US-PGPUB; USPAT; EPO;	OR	OFF	2005/02/01 12:32
<u>.</u>			DERWENT			
L4	3	seladin-1 and prostate	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:33
L5	6	seladin-1	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:33

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2 (bases 1 to 4882)
Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.
Direct Submission
Submitted (24-NOV-1994) Osamu Ohara, Kazusa DNA
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                        Nagase,T., Miyajima,N., Tanaka,A., Sazuka,T., Seki,N., Sato,S., Tabata,S., Ishikawa,K.-i., Kawarabayasi,Y., Kotani,H. and Nomura,N. Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1 NNA RES. 2 (1),.37.43.(1995)
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     Homo sapiens (human)
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D43636
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Patent: WO 01096547-A 47 20-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                   Institute;
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Query Match Best Local Similarity

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CATTCAGCGCATGGTGCTTGGGGACATAGCGGATCGAGACGCCCATTGTAGAAGCCCTGGA

AAAGTATAACATTCCCCTTGTGTCATACAAAAATCTCTCGGAAGAGGAGCACAACAGCAT AAAGTATAACATTCCCCTTGTGTCATACAAAAATCTCTCGGAAGAGGAGCACAACAGCAT TTCTTTAGAAGAGATTGAAAATCATCCTTGGCTTCAGGGAGTGGACCCTTCACCAGCTAC

180

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CATTCAGCGCATGGTGCTTGGGGACATAGCGGATCGAGACGCCATTGTAGAAGCCCTGGA

AGAAAAGCAAGAGAAAGAATACAGACCAGATCTGCAAGCCCGAGCAATATCAAGGCCCA 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                              /cell_type="myeloblast"
/tissue_type="brain"
/clone_Tib="pBluescriptII SK plus"
/note="This sequence was obtained by subcloning of the DNA
fragments derived from two cDNA clones (1 - 1013 was
derived from a RT-PCR product (Lung) and 1014 - 4882 was
derived from ha01240)."
                      RRCAGPSNSMQLASRSAGELVESLKLMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQE
KSTWKMCISSTGNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLCEKT
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                                                                                                                                                                                                                                                                       kinase.
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<1. .2302
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/db_xref="taxon:9606"
            " ISVNIQRNPKEGLLCASSPASCCHVI
                                                                                                                                                                                                                                                                                                    /gene="KIAA0096"
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                                                                                                                                                                                                                                                                                    note="KIAA0096
                                                                                                                                                                                                                                                                                                                                                  . .4882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="ha01240s1"
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Submitted (24-NOV-1994) Osamu Ohara, Kazusa DNA Research Institute;
                                                                                                                                                                                                                                                                                                                                           1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913) On May 9, 2002 this sequence version replaced gi:598957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagase, T., Miyajima, N., Tanaka, A., Sazuka, T., Seki, N., Sato, S., Tabata, S., Ishikawa, K.-i., Kawarabayasi, Y., Kotani, H. and Nomura, N. Prediction of the coding sequences of unidentified human genes. III. The coding sequences of 40 new genes (KIAA00120) deduced by analysis of cDNA clones from human cell line KG-1 DNA_RES_2_(11, 37-43 (1995)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="This sequence was obtained by subcloning of the DNA
fragments derived from two cDNA clones (1 - 1013 was
derived from a RT-PCR product (Lung) and 1014 - 4882 was
derived from ha01240)."
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kinase."
                                                              /gene="KIAA0096"
                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                          /clone="ha01240s1"
                                               . 2302
                                                                                                                                                                                                                           line="KG-1"
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partial cds.
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Query Match
                                                                                                                                                                                                          /codon_start=2
//protein_id="BAA07744.2"
//protein_id="BAA07744.2"
//db_xref="gi:20521878"
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//translation="SMAGFKRGYDGKIAGLYDLDKTLGRGHFAVVKLARHVFTGEKVA
VKVIDKTKLDTLATGHLFQEGVRCMKLVQHPNIVRLYEVIDTQTKLYLILELGDGGDMF
VKVIDKTKLDTLATGHLFQEVRCMKLVQHPNIVRLYEVIDTQTKLYLILELGDGGDMF
VKVIDKTKLDTLAKKYFAQIVHAISYCHKLHVVHRDLKPENVVFFEKQGLVKLTDF
GFSNKRQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFMLVGQDPFQB
DYIMKHEEGGLNEDLAKKYFAQIVHAILGTWARASLEEIBHHFWLQGVDPS
ANDSETLTMINDCKYTVPSHYSKECKOLITMNLQRDPRRARSLEEIBHHFWLQGVDPS
ANDSETLTMINDCKYTVPSHYSKECKOLITMNLQRDPRRARSLEEIBHHFWLQGVDPS
ANTKYNIFLVSYKNLSEEEHNSIIQRWGFRQSWFYXIDVPQOLEDDLTATPLSHATVPLLA
ERILREKQEKEIQTGSASESNIKAQFRQSWFYXIDVPQDLEDDLTATPLSHATVPLAA
ERILREKQEKEIQTGSAKKDDLFBLAGFALSTVPPASLKFTASGRKCLFRVEEDE
PARAADSVLNGHRSKGLCDSAKKDDLFBLAGFALSTVPPASLKFTASGRKCLFRVEEDE
EEDBEDKKPMSLSTQVVLRRKFSVTNRLTSRKSA,PVLAQIFEBGESDDEFDMDEKULP
KLSRLKWNIASFGTVHRRXFSQGRGSSCSSSETSDDDSSERRRLDKNSGFTYSWH
RRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAGGGSPSSGSGAPTNTSGTT
RRCAGPSNSWQLASRSAGELVESLKLMSICLGSQLHGSTKYIIDPQNGLSFSSVVVQE
KSTWKNCISSTGNAGGVPAVGGAIKFFSDHADTTTELERIKSKKNLKNNVLQLPLCEKT
ISVNIQRNPKEGLLCASSPASCCHVI"
          100.0%;
Score 366; DB 9;
Pred. No. 1.4e-64;
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Matches 366; Best Local

Similarity

Conservative

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SOURCE
ORGANISM
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BC071567
LOCUS
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GAAAAACAGTCTIGTATITTTCTGTAIGTGTGTGTGTATATATATATATATTATGTTGCTTCTGGC
                                                                                                                                                                                                                                                                                             5140 bp
Homo sapiens SNF-1 related kinase,
IMAGE:4375623), complete cds.
BC071567
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5140)
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                                                                                                                                                                                                                                                                           BC071567.1 GI:47939483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACAGGTATGTGACAAATGGGAAAAAAAATCCAAATAATAAAGTGACATATTGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACAGGTATGTGACAAATGGGAAAAAAAATCCAAATAATAAAGTGACATATTGGTGTTC
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Matches 400;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G. Gene expression profiles in liver cancer Patent: WO 0229103-A 1609 11-APR-2002; GENE LOGIC INC (US)
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AX828407
AX828407.1
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                                                                                                                           Al-Mahmood,S., Colin,S. and Schneider,C. Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof patent: WO 03074073-A 53 12-SEP-2003;
                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          Gene
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                                                                                                          Signal
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/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No.
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organism="Homo sapiens"
/mol_type="unassigned DN/db_xref="taxon:9606"
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1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913) On Dec 22, 1999 this sequence version replaced gi:285996. Sequence updated (20-Dec-1999).
                                                                                                                                                                                                                       3 (bases 1 to 4187)
Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
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1532-3, Yana, Kisarazu,
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                                                                                                                                                                                                                                      AGAAGACACAAAAAACATCATGATCAACCTGATGGACAT 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="Repaaltarrtmepavslavcallfllmvrlkglefvl1iqqrw
vpvclfflbslifdiyyyrawvvpklssaprlhegwpx10k0yrbwcegsktpm
CTGREGWLTVSLRVGKKKTHKNIMINLBUILEVDTKKQIVAVEFLVLADGSFVRCTDS
IGWTLFVLPELDDLTVGGLIMGTGIESSSHKYGLFQHICTAYELVLADGSFVRCTPSE
IGWTLFVLPELDDLTVGGLIMGTGIESSSHKYGLFQHICTAYELVLADGSFVRCTPSS
IGWTLFVLPELDDLTVGGLIMGTGIESSSHKYGLFQHICTAYELVLADGSFVRCTPSS
IGWTLFVLPELDDLTVGGLIMGTGIESSSHKYGLFQHICTAYELVLADGSFVRCTPSS
IGWTLFVLPWGGCTLGFLVAAEIRIIFAKLKSIGNYYKFWFFKHVENYLKTNTBSQRQEN
HFVEGLLYSLDEAVIMTGVMTDEAFEPSKLNSIGNYYKFWFFKHVENYLKTNTBGLEYI
PLRHYYHRHTRSIFWELQDIIFGNMTJIFFSKLNSIGNYKFWFFKHVENYLKTNTBGLEYI
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PLRHYYHRHTRSIFWELQDIIFGNMTJIFFSKLNSIGNYKFWFKNTBGLEYI
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PLRHYYHRHTRSIFWELQDIIFFSKLNSIGNYKFWFKNTBGLYFWFKNTBGLEYI
PLRHYYHRHTRSIFWELQDIIFFSKLNSIGNYKFWFKNTBGLYFWFKNTBGLYFY
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1590. .>4187
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/protein_id="BAA02806.2"
/db_xref="GI:6630632"
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/cell_line=
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/db_xref="taxon:9606"
/clone="ha005171"
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OS Homo sapiens (human)
PN JP 2002530076-A/1
PD 17-SEP-2002
PF 12-NOV-1999 JP 200058255:
PF 12-NOV-1998 EP 9812147!
PI ROGER NITSCH, ISABELL GREE
PC C12N15/09, A61K38/00, A61K
PC A61P1/00, A61P15/09, A61P.
PC A61P1/00, A61P15/00, A61P.
PC A61P25/28,
PC A61P25/28,
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Methods of diagnosing or treating neurological diseases
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C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
A61P1/00,
A61P11/00, A61P15/00, A61P21/00, A61P25/00, A61P25/14, A61P25/16,
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.7e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayasi, Y., Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S. Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1 (supplement)
                                                                                                                                                                                                                                   Submitted (11-NOV-1992) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913) On Dec 22, 1999 this sequence version replaced gi:285996. Sequence updated (20-Dec-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato,S., Nagase,T., Seki,N., Ishikawa,K. and Tabata,S. Prediction of the coding sequences of unidentified human genes. I The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced analysis of randomly sampled cDNA clones from human immature
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Homo sapiens
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Mammalia; Eutheria;.Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                    Direct Submission
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/gene="KIAA0018"
<1. .1589
                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ha005171"
                                     /cell_type="myoblast"
                                                                                                 /sex="male"
                                                                                                                                                                                                                  ocation/Qualifiers
                                                                              line="KG-1"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausmer, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
                                                                                                                                                                                                                                                                                             שניטען 375 4202 bp mRNA lir
Homo sapiens 24-dehydrocholesterol reductase,
MGC:10569 IMAGE:3638639), complete cds.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 1 (bases 1 to 4202)
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                           BC004375.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTTCTGTTTAAATAAAAGTGGCCTGG 388
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/note="Start codon is not identified. ha00517 cDNA clone for KIAA0018 has a 1-bp deletion at the position 1167 of the sequence of KIAA0018."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLRHYYHRHTRSIFWELQDIIPFGNNPIFRYLFGWMVPPKISLLKLTQGETLRKLYEQ
HHVVQDMLVPMKCLQQALHTFQNDIHVYPIWLCPFILPSQPGLVHPKGNEAELYIDIG
AYGEPRVKHFEARSCMRQLEKFVRSVHGFQMLYADCYMNREEFWEMFDGSLYHKLREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=3
/product="KIAA0018 protein"
/protein_id="BAA02806.2"
/db_xref="GI:6630632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGCQDAFPEVYDKICKAARH"
L590. .>4187
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                                                                                              Feingold, E.A.,
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